Please cancel the present "SEQUENCE LISTING", pages 1-39, and insert therefor the accompanying paper copy of the Substitute Sequence Listing, page numbers 1 to 27, at the end of the application.

## REMARKS

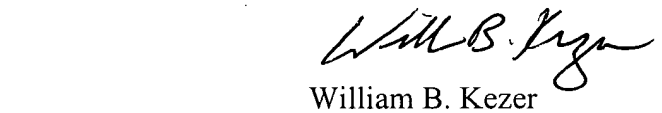
Applicants request entry of this amendment in adherence with 37 C.F.R. §§1.821 to 1.825. This amendment is accompanied by a floppy disk containing the above named sequences, SEQ ID NOS:1-141, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.

The information contained in the computer readable disk was prepared through the use of the software program "FastSEQ" and is identical to that of the paper copy. This amendment contains no new matter.

Attached hereto is a marked-up version of the changes made to the Specification by the current Amendment. The attached pages are captioned "**VERSION WITH MARKINGS TO SHOW CHANGES MADE.**"

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,



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## VERSION WITH MARKINGS TO SHOW CHANGES MADE

**In the Specification:**

Paragraph beginning at line 9 of page 15 has been amended as follows:

The longer chain portion can be any of a variety of molecules which are inert to the subsequent conditions necessary for attaching the oligonucleotide probes, or for hybridization of a sample to the probe array. These longer chain portions will typically be ethylene glycol oligomers containing 2-14 monomer units, diamines, diacids, amino acids, peptides, or combinations thereof. In some embodiments, the longer chain portion is a polynucleotide (*e.g.*, a 15-mer of poly dT; SEQ ID NO:141). Additionally, for use in synthesis of the probe arrays, the linking group will typically have a protecting group, attached to a functional group (*i.e.*, hydroxyl, amino or carboxylic acid) on the distal or terminal end of the chain portion (opposite the solid support). After deprotection and coupling, the distal end is covalently bound to an oligonucleotide probe (*e.g.*, an HLA Class I oligonucleotide probe).

Paragraph beginning at line 24 of page 16 has been amended as follows:

The length of the spacer between the support and the hybridization sequence influences the efficiency of hybridization (Guo et al, *Nuc. Acids Res.* **22**:5456-5465 (1994)). When large DNA fragments, such as PCR products, are allowed to hybridize with short oligonucleotide probes immobilized on solid supports, adequate distance between the hybridization sequence and the solid surface is required in order to achieve the efficient hybridization. This is due to the steric interference between large DNA molecules and the support. Within one embodiment of the invention, a 15-mer dT spacer (SEQ ID NO:141) was employed in each oligonucleotide probe to provide

adequate space between hybridization sequence and the support. Although requiring extra expense in oligonucleotide synthesis, the 15-mer spacer was essential to optimize hybridization signals. Each completed probe contained a 5' amino group for immobilization chemistry, a 20-nucleotide hybridization sequence, and a 15-mer dT spacer (SEQ ID NO:141) between them.

Paragraph beginning at line 3 of page 28 has been amended as follows:

Once the solid support has been suitably derivatized, a linking group is attached to provide a spacing between the oligonucleotide probe and the support which is optimized for interactions between the probes and the sample. As provided above, a variety of linking groups can be used in this aspect of the invention. Preferred groups are those that provide a spacing similar to that provided by a 15-mer poly dT spacing group (SEQ ID NO:141). Additionally, the linking group will have a reactive portion that is selected to be compatible with the amino group of the aminoalkylsilane-derivatized support, or with the functional group present on the reagent used to facilitate linking group attachment (*e.g.,* the isothiocyanate portion of 1,4-phenylenediisothiocyanate). Accordingly, at the proximal end (that forming an attachment closest to the support), the linking group will have a functional group that is reactive with an amino moiety (*e.g.*, a carboxylic acid, anhydride, isothiocyanate, and the like) or a functional group that is reactive with an isocyanate, isothiocyanate or carboxylic acid moiety (*e.g.,* an amino group, a hydroxyl group or the like).

Paragraph beginning at line 17 of page 28 has been amended as follows:

In a particularly preferred embodiment, the support is derivatized first with aminopropyltrimethoxysilane, followed by attachment of 1,4-phenylenediisothiocyanate, followed by attachment of a 15-mer oligonucleotide, preferably a 15-mer of poly-dT (SEQ ID NO:141).

Paragraph beginning at line 1 of page 37 has been amended as follows:

Exon 2 of HLA-B gene was amplified by two-step asymmetric PCR. In the first step, the PCR primers were Exon 2 5'-primer (5'-GCTCCCACTCCATGAGGTAT-3'; SEQ ID NO:71 ~~SEQ ID NO: 138~~) and Exon 2 3'-primer (5'-CGGCCTCGCTCTGGTTGTAG-3'; SEQ ID NO:138 ~~SEQ ID NO:139~~). The one hundred microliter amplification reaction contained 50 mM KCl, 10 mM Tris-HCl, 1.5 mg MgCl2, 10 mg of gelatin, 20 ng of genomic DNA, 2 microMoles of each primer, 200 microMoles each of dATP, dCTP, dTTP and dGTP, and 2.5 U of Taq DNA polymerase. The amplification reaction was performed in a Perkin-Elmer Cetus 9600 thermal cycler using 35 cycles of the following profile: 94°C for 30 seconds, 60°C for 1 minute and 72°C for 1 minute. The PCR mixture was then purified using a QIAGEN PCR purification kit (QIAGEN Inc., Chatsworth, CA) to remove the excess primers. In the second step, the PCR primer employed was a 5' Rhodamine-labeled Exon 2 3'-primer (SEQ ID NO:138) ~~(SEQ ID NO 139)~~. The PCR was performed in 30 cycles using the following profile: 94°C for 30 seconds, 60°C for 1 minute and 72°C for 2 minutes.

Paragraph beginning at line 14 of page 37 has been amended as follows:

Amplification of exon 3 of HLA-B was accomplished using Exon 3 5'-primer (5'-ACCCGGTTTCATTTTCAGTTG-3'; SEQ ID NO:139 ~~SEQ ID NO:140~~) and Exon 3 3'-primer (5'-CCCACTGCCCCTGGTACC-3'; SEQ ID NO:140 ~~SEQ ID NO:141~~). The ampification reaction was performed in 35 cycles of the following profile: 94°C for 30 seconds, 65°C for 1 minute and 72°C for 1 minute. To generate single-strand exon 3 product, the second PCR was performed, employing a 5' Rhodamine-labeled 3 3'-primer (SEQ ID NO:140) ~~(SEQ ID NO:141)~~, in 30 cycles of the following profile: 94°C for 1 minute, 65°C for 1 minute and 72°C for 2 minutes ~~minute~~.